A NOTE ON SYSTEM MODELLING, AGGREGATION AND REDUCTIONISM

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SUMMARY

Zeigler and Weinberg (1970) *presented a system theoretic discussion of biological modelling. In this paper some implications of this formulation for the wider problem of reductionism are examined. It is argued that the reduction of biology to physics, for example, involves a relation between co-ordinates typical of biological models and those typical of quantum-mechanical models. This relation is shown to be rather special and not empirically or methodologically necessary.*

SOMMAIRE

Zeigler et Weinberg (1970) *ont présenté une discussion théorique du système de modèlement biologique. Dans cette étude quelques-unes des implications de cette formulation pour le problème plus étendu de réductionisme sont examinées. L'on atteste que la réduction de la biologie à la physique, par exemple, entraîne une relation entre les co-ordinées qui sont typiques de modèles biologiques et celle qui sont typiques de modèles quanto-mécaniques. L'on indique que cette relation est assez spéciale et pas nécessaire empiriquement ou méthodologiquement.*

Zeigler and Weinberg (1970) argued that a relatively simple system is a model of a more complex one if the two can be placed in a homomorphic relation. Such a homomorphism is a mapping between the state spaces of the two systems which preserves their transition functions and thus enables their state behaviours to be correlated in a time invariant manner.

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Thus making a model of a system involves two activities: (1) constructing the model itself, *i.e.* the system which is intended to be a homomorphic image, and (2) determining whether such a homomorphism actually exists. For example one may start with two systems whose structure is (at least partially) known and then look for mappings which establish that the systems are homomorphic. This occurs when one seeks analogues for systems. Usually, however, in modelling and for computer simulation it is the mapping between state spaces which is determined at the beginning, and a transition function is sought for the model which establishes this mapping as a homomorphism.

That is to say, the mapping is usually implicit in the kinds of measurements that will be made on the system to be modelled and one attempts to arrive at an adequate structure for the model by comparing the behavioural output of the model (obtained analytically or by simulation) with the behaviour of the measured system.

This is illustrated in the activities which brought our model of the living cell into being (Zeigler and Weinberg, 1970; Weinberg, 1970). We decided to partition the chemicals found in the cell into blocks (or pools as we call them) and our model uses these pools as co-ordinates (or unitary entities). This amounts to a specification of the mapping between the real cell and the model, since the adequacy of the model can be established only by comparing the behaviours of these pools with similar measurements obtained from real cells. Once the selection of a mapping and state space were made, the search for an adequate transition function could begin.

The aggregation technique used in our model, while commonly employed in social system simulations, is quite novel in bio-simulation. Its nature has not been well understood and there have arisen disputes concerning whether models obtained in this way are truly in the scientific tradition or are mere expedients which, though useful for certain limited purposes, do not contribute to basic scientific knowledge.

In considering this issue we assert that all models derive their validity by being homomorphic rather than isomorphic representations. In particular the complexity of a model, as measured for example by the storage and running time demands of its computer program realisation, must be limited if it is to be the basis of a realistic computer simulation.

Aggregation or co-ordinate lumping is a particular technique for reducing the complexity of a model. Our mathematical formulation (Zeigler and Weinberg, 1970) has shown that it can indeed reduce both the storage and time complexity of a model at the same time (it need not decrease one at the expense of the other). Moreover not all co-ordinate partitions can result in homomorphic image systems—the condition of preservation of co-ordinate functionality must be satisfiable in the state space determined by the lumped co-ordinates.

Finally, an important feature of the homomorphic systems derived by aggregation is that more than just the state behaviour can be preserved: the local structure of interaction of co-ordinates can also be preserved.

Aggregation as a metaphysic in science has been well described by Bohm (1969).

If one accepts the assumption that the universe is basically composed of particles moving according to the laws of physics then

> 'it follows that the whole order of behavior of any system of particles is in reality determined completely by the mechanical order of movement of constituent particles. To be sure, one may find it convenient to group these particles into systems, such as atoms, molecules, cells, organs, organisms, etc. Because these particles interact with each other, the systems can display a sort of "collective behavior" in which they "work together" in a general overall way as a kind of relatively stable unit on a higher level. As a result, one can simplify things by abstracting from the basic laws a suitable partial treatment of the order in which these systems move.'

It is interesting to note that a possible explication of the way in which blocks of particles must 'work together' to display 'collective behaviour' is that the condition of preservation of co-ordinate functionality is satisfiable in the space spanned by the state sets of these blocks. In this case, and only in this case, can behaviour in this state space be correlated to the behaviour of the basic particle system in a time-invariant manner. It is in this sense that we might understand how groups of particles display 'collective behaviour'.

Bohm and others, *e.g.* Polanyi (1968), argue against the reductionist assumption that all behaviour is determined at the basic particle level and nothing new need be known in principle to predict behaviour at the higher levels. Supporters and attackers of this position both seem to make a more fundamental assumption whose existence becomes apparent when this problem is considered from a systems viewpoint. This assumption is that *the co-ordinate sets of models can be placed in a simple linear order in which the co-ordinates of any model at one level are aggregates of the co-ordinates at lower levels.* Moreover, the hierarchy so generated is assumed to have a lowest level which is usually taken to be the atomic level.

Even granting the possibility of such a hierarchy, there is, according to nuclear physics, a very real problem of whether a lowest level in fact exists. But even more fundamentally, there is nothing *a priori* to suggest that co-ordinate sets need necessarily fall into so simple an order. True enough one can order co-ordinate sets according to whether one set is obtained by aggregation of another, but the order so obtained is a *partial* order, *i.e.* many pairs of co-ordinate sets will not be comparable in the way.

We might note here that even if the co-ordinate sets of a pair of models can be straightforwardly related, one requires in addition a set of computable mappings which relate the *state* sets of the co-ordinates (this set of mappings constitutes the homomorphism relating the two systems). Rosen (1969) has emphasised this latter requirement for a reductionist program.

Examined in this light, the assumption of a linear order amounts to the claim that the co-ordinate sets for some special class of models must fall into a linear

order. Such a class might be the class of models actually employed by scientists or of ultimate utility to science, etc. For example, one might claim that a model is not truly scientific unless one can see how to interpret its entities as aggregates of atoms, for only in this way, it would be claimed, can one account for the assumed properties of the entities.

In actual fact there are many models employed in biology and other sciences whose co-ordinate sets are apparently incomparable with the atomic co-ordinates. I have argued that the validity of such models can be judged by the extent to which they are homomorphic images of the real system intended to be modelled. From this point of view, the atomic model, *i.e.* the quantum-mechanical theory, is no more basic than any other; it is a highly confirmed model adequately accounting for a limited range of phenomena. Thus any restriction on the kinds of entities that models can be based upon is an additional criterion which is beside the point as far as the validity of the model is concerned. One may sympathise with the desire to attain unity in science by restrictions of this kind, but there is no necessity, logical or practical, that unity of this hierarchical kind exists.

We see that the debate concerning the reductionist assumption becomes meaningful only if one accepts the more basic assumption that models of real systems fall into a linear order. If belief in the latter assumption is unfounded, and we have argued that it is, it follows that both sides in the controversy must re-examine their premises before re-joining the debate.

Of course, we are not arguing that the concept of aggregation, when applicable, is not valuable in linking entities at the various levels of organisation. On the contrary, this paper has noted the utility of the aggregation process in complexity reduction. We caution only that entities as co-ordinates of valid models are not, of necessity, related in this way.

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